

RAW SEQUENCE LISTING

The Biotechnology Systems Branch of the Scientific and Technical Information Center (STIC) no errors detected.

Application Serial Number: 19585, 964
Source: IFWP
Date Processed by STIC: 7/25/06

ENTERED



IFWP

RAW SEQUENCE LISTING

DATE: 07/25/2006

PATENT APPLICATION: US/10/585,964

TIME: 15:09:31

Input Set : A:\NEB-236-PUS.ST25.txt

Output Set: N:\CRF4\07252006\J585964.raw

```

3 <110> APPLICANT: New England Biolabs, Inc.
4     Guan, Chudi
5     Kumar, Sanjay
6     Kucera, Rebecca
8 <120> TITLE OF INVENTION: Modified DNA Cleavage Enzymes and Methods of Use (as amended
by
9     ISA)
11 <130> FILE REFERENCE: NEB-236-PUS
C--> 13 <140> CURRENT APPLICATION NUMBER: US/10/585,964
C--> 13 <141> CURRENT FILING DATE: 2006-07-13
13 <150> PRIOR APPLICATION NUMBER: 60/524,123
14 <151> PRIOR FILING DATE: 2003-11-21
16 <150> PRIOR APPLICATION NUMBER: PCT/US04/039288
17 <151> PRIOR FILING DATE: 2004-11-22
19 <160> NUMBER OF SEQ ID NOS: 25
21 <170> SOFTWARE: PatentIn version 3.2
23 <210> SEQ ID NO: 1
24 <211> LENGTH: 450
25 <212> TYPE: DNA
26 <213> ORGANISM: unknown
28 <220> FEATURE:
29 <223> OTHER INFORMATION: enterobacteria phage T7
31 <400> SEQUENCE: 1
32 atggcaggtt acggcgctaa aggaatccga aaggttggag cgtttcgctc tggcctagag      60
34 gacaaggttt caaagcagtt ggaatcaaaa ggtattaaat tcgagtatga agagtggaaa      120
36 gtgccttatg taattccggc gagcaatcac acttacactc cagacttctt acttccaaac      180
38 ggtatattcg ttgagacaaa gggctctgtgg gaaagcgatg atagaaagaa gcacttatta      240
40 attagggagc agcaccgccg gctagacatc cgtattgtct tctcaagctc acgtactaag      300
42 ttatacaaaag gttctccaac gtcttatgga gagttctgcg aaaagcatgg tattaagttc      360
44 gctgataaac tgatacctgc tgagtggata aaggaaccca agaaggaggt cccctttgat      420
46 agattaaaaa ggaaaggagg aaagaaataa                                450
49 <210> SEQ ID NO: 2
50 <211> LENGTH: 27
51 <212> TYPE: DNA
52 <213> ORGANISM: artificial
54 <220> FEATURE:
55 <223> OTHER INFORMATION: primer
57 <400> SEQUENCE: 2
58 cccgaattca tggcaggtta cggcgct                                27
61 <210> SEQ ID NO: 3
62 <211> LENGTH: 27
63 <212> TYPE: DNA
64 <213> ORGANISM: artificial
66 <220> FEATURE:

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67 <223> OTHER INFORMATION: primer
69 <400> SEQUENCE: 3
70 cccccaagct tatttctttc ctccttt 27
73 <210> SEQ ID NO: 4
74 <211> LENGTH: 30
75 <212> TYPE: DNA
76 <213> ORGANISM: unknown
78 <220> FEATURE:
79 <223> OTHER INFORMATION: primer
81 <400> SEQUENCE: 4
82 tggaagtaag aagtctggcc actcttcata 30
85 <210> SEQ ID NO: 5
86 <211> LENGTH: 30
87 <212> TYPE: DNA
88 <213> ORGANISM: artificial
90 <220> FEATURE:
91 <223> OTHER INFORMATION: primer
93 <400> SEQUENCE: 5
94 ttcgagtatg aagagtggcc agacttctta 30
97 <210> SEQ ID NO: 6
98 <211> LENGTH: 39
99 <212> TYPE: DNA
100 <213> ORGANISM: unknown
102 <220> FEATURE:
103 <223> OTHER INFORMATION: oligonucleotide
105 <400> SEQUENCE: 6
106 aaagtcctt atgtaattgc gagcaatcac acttacact 39
109 <210> SEQ ID NO: 7
110 <211> LENGTH: 39
111 <212> TYPE: DNA
112 <213> ORGANISM: unknown
114 <220> FEATURE:
115 <223> OTHER INFORMATION: oligonucleotide
117 <400> SEQUENCE: 7
118 agtgaagtg tgattgcacg caattacata aggcacttt 39
121 <210> SEQ ID NO: 8
122 <211> LENGTH: 36
123 <212> TYPE: DNA
124 <213> ORGANISM: unknown
126 <220> FEATURE:
127 <223> OTHER INFORMATION: oligonucleotide
129 <400> SEQUENCE: 8
130 aaagtcctt atgtaattag caatcacact tacact 36
133 <210> SEQ ID NO: 9
134 <211> LENGTH: 36
135 <212> TYPE: DNA
136 <213> ORGANISM: unknown
138 <220> FEATURE:
139 <223> OTHER INFORMATION: oligonucleotide

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141 <400> SEQUENCE: 9
142 agtgtaagtg tgattgctaa ttacataagg cacttt      36
145 <210> SEQ ID NO: 10
146 <211> LENGTH: 40
147 <212> TYPE: DNA
148 <213> ORGANISM: unknown
150 <220> FEATURE:
151 <223> OTHER INFORMATION: oligonucleotide mixture
154 <220> FEATURE:
155 <221> NAME/KEY: misc_feature
156 <222> LOCATION: (24)..(24)
157 <223> OTHER INFORMATION: n is a, c, g, or t
159 <400> SEQUENCE: 10
W--> 160 aaagtgcctt atgtaaattc ccantaatca cacttacact      40
163 <210> SEQ ID NO: 11
164 <211> LENGTH: 40
165 <212> TYPE: DNA
166 <213> ORGANISM: unknown
168 <220> FEATURE:
169 <223> OTHER INFORMATION: oligonucleotide mixture
172 <220> FEATURE:
173 <221> NAME/KEY: misc_feature
174 <222> LOCATION: (17)..(17)
175 <223> OTHER INFORMATION: n is a, c, g, or t
177 <400> SEQUENCE: 11
W--> 178 agtgtaagtg tgattantgg gaatttacat aaggcacttt      40
181 <210> SEQ ID NO: 12
182 <211> LENGTH: 149
183 <212> TYPE: PRT
184 <213> ORGANISM: unknown
186 <220> FEATURE:
187 <223> OTHER INFORMATION: enterobacteria phage T7
189 <400> SEQUENCE: 12
191 Met Ala Gly Tyr Gly Ala Lys Gly Ile Arg Lys Val Gly Ala Phe Arg
192 1          5          10          15
195 Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Ser Lys Gly Ile
196          20          25          30
199 Lys Phe Glu Tyr Glu Glu Trp Lys Val Pro Tyr Val Ile Pro Ala Ser
200          35          40          45
203 Asn His Thr Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe Val
204          50          55          60
207 Glu Thr Lys Lys Gly Leu Trp Glu Ser Asp Asp Arg Lys Lys His Leu Leu
208 65          70          75          80
211 Ile Arg Glu Gln His Pro Glu Leu Asp Ile Arg Ile Val Phe Ser Ser
212          85          90          95
215 Ser Arg Thr Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Gly Glu Phe
216          100         105         110
219 Cys Glu Lys His Gly Ile Lys Phe Ala Asp Lys Leu Ile Pro Ala Glu
220          115         120         125

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223 Trp Ile Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Arg Leu Lys Arg
224      130                      135                      140
227 Lys Gly Gly Lys Lys
228 145
231 <210> SEQ ID NO: 13
232 <211> LENGTH: 151
233 <212> TYPE: PRT
234 <213> ORGANISM: unknown
236 <220> FEATURE:
237 <223> OTHER INFORMATION: yersinia pestis phage phiA1122
239 <400> SEQUENCE: 13
241 Met Ala Gly Thr Tyr Ala Ala Arg Gly Ile Arg Lys Val Gly Thr Phe
242 1                      5                      10                      15
245 Arg Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Gly Lys Gly
246      20                      25                      30
249 Ile Lys Phe Asp Tyr Glu Leu Trp Lys Ile Pro Tyr Val Val Pro Ala
250      35                      40                      45
253 Ser Asn His Val Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe
254      50                      55                      60
257 Ile Glu Thr Lys Gly Leu Trp Glu Ser Asp Asp Arg Lys Lys His Leu
258 65                      70                      75                      80
261 Leu Ile Arg Glu Gln Phe Pro Glu Leu Asp Ile Arg Leu Val Phe Ser
262      85                      90                      95
265 Ser Ser Arg Thr Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Gly Glu
266      100                     105                     110
269 Trp Cys Glu Lys His Gly Ile Leu Phe Ala Asp Lys Leu Ile Pro Val
270      115                     120                     125
273 Glu Trp Leu Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Arg Leu Lys
274      130                     135                     140
277 Gln Ala Lys Gly Gly Lys Lys
278 145                     150
281 <210> SEQ ID NO: 14
282 <211> LENGTH: 153
283 <212> TYPE: PRT
284 <213> ORGANISM: unknown
286 <220> FEATURE:
287 <223> OTHER INFORMATION: bacteriophage phiYe03-12
289 <400> SEQUENCE: 14
291 Met Ala Gly Ala Tyr Ala Ala Arg Gly Val Arg Lys Val Gly Ala Phe
292 1                      5                      10                      15
295 Arg Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Ser Lys Gly
296      20                      25                      30
299 Ile Lys Phe Asp Tyr Glu Leu Trp Arg Ile Pro Tyr Val Ile Pro Ala
300      35                      40                      45
303 Ser Asp His Leu Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe
304      50                      55                      60
307 Ile Glu Thr Lys Gly Leu Trp Asp Ser Asp Asp Arg Lys Lys His Leu
308 65                      70                      75                      80
311 Leu Ile Arg Glu Gln His Pro Glu Leu Asp Ile Arg Leu Val Phe Ser

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```

312          85          90          95
315 Ser Ser Arg Ser Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Ala Glu
316          100          105          110
319 Trp Cys Glu Lys His Gly Ile Leu Phe Ala Asp Lys Leu Ile Pro Val
320          115          120          125
323 Glu Trp Leu Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Lys Phe Lys
324          130          135          140
327 Thr Lys Lys Gly Val Lys Lys Asn Gly
328 145          150
331 <210> SEQ ID NO: 15
332 <211> LENGTH: 152
333 <212> TYPE: PRT
334 <213> ORGANISM: Bacteriophage T3
336 <400> SEQUENCE: 15
338 Met Ala Gly Ala Tyr Ala Ala Arg Cys Thr Gln Gly Arg Ala Phe Arg
339 1          5          10          15
342 Ser Gly Leu Glu Asp Lys Val Ser Lys Gln Leu Glu Ser Lys Gly Ile
343          20          25          30
346 Lys Phe Asp Tyr Glu Leu Trp Arg Ile Pro Tyr Val Ile Pro Glu Ser
347          35          40          45
350 Asp His Leu Tyr Thr Pro Asp Phe Leu Leu Pro Asn Gly Ile Phe Ile
351          50          55          60
354 Glu Thr Lys Lys Gly Leu Trp Asp Ser Asp Asp Arg Lys Lys His Leu Leu
355 65          70          75          80
358 Ile Arg Glu Gln His Pro Glu Leu Asp Ile Arg Leu Val Phe Ser Ser
359          85          90          95
362 Ser Arg Ser Lys Leu Tyr Lys Gly Ser Pro Thr Ser Tyr Gly Glu Trp
363          100          105          110
366 Cys Glu Lys His Gly Ile Leu Phe Ala Asp Lys Leu Ile Pro Val Ala
367          115          120          125
370 Gly Val Lys Glu Pro Lys Lys Glu Val Pro Phe Asp Lys Phe Lys Thr
371          130          135          140
374 Lys Lys Gly Val Lys Lys Asn Gly
375 145          150
378 <210> SEQ ID NO: 16
379 <211> LENGTH: 147
380 <212> TYPE: PRT
381 <213> ORGANISM: unknown
383 <220> FEATURE:
384 <223> OTHER INFORMATION: pseudomonas phage gh-1
386 <400> SEQUENCE: 16
388 Met Ala Tyr Ala Gly Pro Lys Gly Ala Arg Thr Gly Ala Phe Arg Ser
389 1          5          10          15
392 Gly Leu Glu Asp Arg Asn Ala Lys His Met Asp Lys Leu Gly Val Lys
393          20          25          30
396 Tyr Asp Phe Glu Arg Phe His Ile Asn Tyr Val Val Pro Ala Arg Asp
397          35          40          45
400 Ala Lys Tyr Thr Pro Asp Phe Val Leu Ala Asn Gly Ile Ile Ile Glu
401          50          55          60

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RAW SEQUENCE LISTING ERROR SUMMARY
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Please Note:

Use of n and/or Xaa have been detected in the Sequence Listing. Please review the Sequence Listing to ensure that a corresponding explanation is presented in the <220> to <223> fields of each sequence which presents at least one n or Xaa.

Seq#:10; N Pos. 24
Seq#:11; N Pos. 17

Invalid <213> Response:

Use of "Artificial" only as "<213> Organism" response is incomplete, per 1.823(b) of New Sequence Rules. Valid response is Artificial Sequence.

Seq#:2,3,5

VERIFICATION SUMMARY

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Input Set : A:\NEB-236-PUS.ST25.txt

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L:13 M:270 C: Current Application Number differs, Replaced Current Application No
L:13 M:271 C: Current Filing Date differs, Replaced Current Filing Date
L:160 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:10 after pos.:0
L:178 M:341 W: (46) "n" or "Xaa" used, for SEQ ID#:11 after pos.:0